STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/520,033
Source: PCT/10
Date Processed by STIC: 1/10/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 10/520,033

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

PCT

RAW SEQUENCE LISTING DATE: 01/10/2006
PATENT APPLICATION: **US/10/520,033** TIME: 08:16:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

see item 2 on Error Summary Sheet

3 <110> APPLICANT: Chan, Raquel
5 <120> TITLE OF INVENTION: Transcription factor gene induced by water deficit conditions and
6 abscisic acid from Helianthus annuus, promoter and transgenic plants
8 <130> FILE REFERENCE: US PCT
C--> 10 <140> **CURRENT APPLICATION NUMBER: US/10/520,033**
C--> 10 <141> **CURRENT FILING DATE: 2004-12-30**
10 <160> NUMBER OF SEQ ID NOS: 22
12 <170> SOFTWARE: PatentIn version 3.1

these lines exceed 72 characters

see pp 1-6

ERRORED SEQUENCES

delete all alphabetical headings

Does Not Comply
Corrected Diskette Needed

E--> 14 <210> ~~SEQ ID NO:1~~ 1 ← just show "1"

do NOT use alphabetical headings in a "new" sequence

15 <211> LENGTH: 774
16 <212> TYPE: DNA
17 <213> ORGANISM: Helianthus annuus
OK--> 19 <400> **SEQUENCE: 1**
20 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg 60
22 tctcttcaac aagtacccac aacagaaaca accaccagga agaaccgaaa cgaggggcgg 120
24 aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga 180
26 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg 240
28 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat 300
30 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag 360
32 aatcaggccc tactcaatca ggtatggttg caaacttaca atgttgcatt caactattta 420
34 agtagttttg aatttttgtg acaataaaga ttgacaaatg ttgtttgata attgattaac 480
36 agttggaggt gctgagaaat gtagcagaaa agcatcaaga gaaaactagt agtagtggca 540
38 gcggtgaaga atcggatgat cggtttacga actctccgga cgttatgttt ggtcaagaaa 600
40 tgaatgttcc gttttgcgac ggttttgcgt actttgaaga aggaaacagt ttgttggaga 660
42 ttgaagaaca actgccagac cctcaaaagt ggtgggagtt ctaaagagta aagaaggatg 720
44 tagaagtagt agagtaaaaa ctaaaacata ccagatagtt ggtttacact ttgt 774

Rules for correct sequence listing

E--> 47 <210> ~~SEQ ID NO:~~ 2
48 <211> LENGTH: 673
49 <212> TYPE: DNA
50 <213> ORGANISM: Helianthus annuus
OK--> 52 <400> **SEQUENCE: 2**
53 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg 60
55 tctcttcaac aagtacccac aacagaaaca accaccagga agaaccgaaa cgaggggcgg 120
57 aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga 180
59 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg 240
61 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat 300
63 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag 360
65 aatcaggccc tactcaatca gttggaggtg ctgagaaatg tagcagaaaa gcatcaagag 420
67 aaaactagta gtagtggcag cggtgaagaa tcggatgatc ggtttacgaa ctctccggac 480

RAW SEQUENCE LISTING DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033 TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

gttatgtttg gtcaagaaat gaatgttccg ttttgcgacg gttttgcgta ctttgaagaa 540
ggaaacagtt tgttggagat tgaagaacaa ctgccagacc ctcaaaagtg gtgggagttc 600
taaagagtaa agaaggatgt agaagtagta gagtaaaaac taaaacatac cagatagttg 660
gtttacactt tgt 673

E--> <210> SEQ ID NO 3
<211> LENGTH: 1221
<212> TYPE: DNA
<213> ORGANISM: Helianthus annuus
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(1221)
<223> OTHER INFORMATION: Large allele

E--> <400> SEQUENCE: 3
gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca 60
caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc 120
atattaaaag tagtagcccc cacccccatt tgttacctac catttcccac tttaataatc 180
acccacgcta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa 240
ccaaattttt tttagtggaa aacaaattcc ccaaatagaa tactaacgaa attcatcgca 300
tcagaataca ctcatctctg aacagtggcg aagcttgacg ttttcgacgg ggggtcggaa 360
aacgtatgta cccgaaattt ctatagaatc ggggggtcga aaacgtatat acccaaaatt 420
tctatacgaa aactacatat ataacactac tgagcaaaaa gttcgggggt tcgggcgccc 480
ctcccggccc cttcaaagct tcgccaatgt ctctgaaccg aagaaaaccc tcactcgtct 540
actagccaat gaatcctcac cagggaaacc ctcactcgtc ttactggact attggcgctt 600
ccaaatggac tacttgcgaa attcaccaca tcgggataca ctcgtctact gcggtgaggt 660
aaaacccgct tggctcaagg atcgaactag cgattgctgc ctactcgcct aatctcccat 720
catcaacagg tgccgccgaa acaaaatgct gggggcggga gttgaaccta ggtccagtga 780
cgcacccatg aatttttttt ctagggatgc gaacgagtgg tttaaccata cttttaagag 840
gtgcgatcgg aaattttacc tataaaatac actaaaaaag ttccaagggt ccacccaccc 900
cttaacctaa gtccgccttt gtctggatca cgtgaaacat caggtctctc ccttaccagt 960
ccagctacga ctcattgaca aaatatcaaa accatatgat tttgagtttt atctcaaccg 1020
aaagtgacat catgacagag aatcgacata accaaaacgt gtaaacgtac aactcaccat 1080
tgcgttgaaa aggacaaaac aggtaggatt cttgtcaaat tcaacgcgta cacctgtgct 1140
tcatctaaac cccatacttt aagaaccttt ataaagacca ctcactatat atacacatat 1200
ataatatcac ttatcaaacc c 1221

E--> <210> SEQ ID NO 4
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having Hind I
II site

E--> <400> SEQUENCE: 4
gcgaagcttg atgcgaacga gtggttta 28

E--> <210> SEQ ID NO 5
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having Sal I

RAW SEQUENCE LISTING DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033 TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

153 site
E--> 155 <400> SEQUENCE: 5
156 gcggtcgaca cctggcacat cgtatctt 28
E--> 159 <210> SEQ ID NO 6
160 <211> LENGTH: 27
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having Bam HI
166 site
E--> 168 <400> SEQUENCE: 6
169 cgcggatccg agggtttgat aagtgat 27
E--> 172 <210> SEQ ID NO 7
173 <211> LENGTH: 27
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having Hind I
179 II site
E--> 181 <400> SEQUENCE: 7
182 cccaagctta acctaagtcc gcctttg 27
E--> 185 <210> SEQ ID NO 8
186 <211> LENGTH: 27
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having Hind II
192 I site
E--> 194 <400> SEQUENCE: 8
195 ggcaagctta tctcaaccga aagtgac 27
E--> 198 <210> SEQ ID NO 9
199 <211> LENGTH: 19
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Designed oligonucleotide based on the 5' promoter
E--> 206 <400> SEQUENCE: 9
207 atttcgcaag tagtccatt 19
E--> 210 <210> SEQ ID NO 10
211 <211> LENGTH: 1015
212 <212> TYPE: DNA
213 <213> ORGANISM: Helianthus annuus
E--> 215 <400> SEQUENCE: 10
216 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca 60
218 caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc 120
220 atattaaaag tagtagcccc cacccccatt tgttacctac catttcccac tttaataatc 180
222 acccacgcta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa 240
224 ccaaattttt tttaatggaa aacaaatact tcaaatgcac tattggtgaa attcaccaca 300
226 tcagaataca cccgtctcta ctcatctact ggccaacgaa tcttcacggg ggaaaccctc 360

RAW SEQUENCE LISTING DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033 TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

228 actcgtctac tgggactact ggcgcttcaa aatggactac tgacaaaatt caccacatcg 420
230 ggatacactt gtctactgcg gtgaggtaaa atccgccgct cagctcaatg atcgaactag 480
232 cgatcgccac ccactcacct tgtctcccat catcaccagg tgccgccaaa acaaaatgtt 540
234 gggggcggga attgaaccta ggtccagtgg cgcacccatg aatttttttt ctagggatgc 600
236 gaacgagtga tttaaccata cttttaagag gtgcgatcgg aaatttttacc tataaaatat 660
238 actaaaaaaa tttcaagggt ccgcccaccc acccccttaac ctaagtccgc ctctgcctgg 720
240 atcacgtgaa acatcaggtc tctctcttac cagttcacct acaactcatt gacaaaatat 780
242 caaaaccata tgattttgag ttttatctca accgaaagtg acatcatgac agagaatcga 840
244 cataaccaaa acgtgtaaac gtacaactca ccattgcgtt gaaaaggaca aaacaggtag 900
246 gattcttgtc aaattcaacg cgtacacctg tgcttcatct aaaccccata ctttaagaac 960
248 ctttataaag accactcact atatatacac atatataata tcacttatca aaccc 1015

E--> 251 <210> SEQ ID NO: 11
252 <211> LENGTH: 28
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Designed oligonucleotide that matches nucleotides 81-100 of the H
258 ahb-4 cDNA sequence and having Bam HI site
E--> 260 <400> SEQUENCE: 11
261 ggcggatcca acagaaacaa ccaccagg 28

E--> 264 <210> SEQ ID NO: 12
265 <211> LENGTH: 29
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Designed oligonucleotide for cloning 5' cDNA and having Bam HI s
271 ite
E--> 273 <400> SEQUENCE: 12
274 ggcggatccc ctggtggttg tttctgttg 29

E--> 277 <210> SEQ ID NO: 13
278 <211> LENGTH: 34
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial
282 <220> FEATURE:
283 <223> OTHER INFORMATION: oligonucleotide based on 5' cDNA and having Xho I site
E--> 285 <400> SEQUENCE: 13
286 gaggactcga gctcaagttt ttttttttt tttt 34

E--> 289 <210> SEQ ID NO: 14
290 <211> LENGTH: 18
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Oligonucleotide based on 5' cDNA and having Xho I site
E--> 297 <400> SEQUENCE: 14
298 gaggactcga gctcaagc 18

E--> 301 <210> SEQ ID NO: 15
302 <211> LENGTH: 29
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033 TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

306 <220> FEATURE:
307 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having Eco RI
308 site
E--> 310 <400> SEQUENCE: 15
311 gccgaattca gattgagcaa gagtataac 29
E--> 314 <210> SEQ ID NO: 16
315 <211> LENGTH: 19
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
E--> 322 <400> SEQUENCE: 16
323 acctttataa agaccactc 19
E--> 326 <210> SEQ ID NO: 17
327 <211> LENGTH: 19
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
E--> 334 <400> SEQUENCE: 17
335 acgcaatggt gagttgtac 19
E--> 338 <210> SEQ ID NO: 18
339 <211> LENGTH: 24
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial
343 <220> FEATURE:
344 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
E--> 346 <400> SEQUENCE: 18
347 aattcagatc tcaataattg agag 24
E--> 350 <210> SEQ ID NO: 19
351 <211> LENGTH: 24
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial
355 <220> FEATURE:
356 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
E--> 358 <400> SEQUENCE: 19
359 gatcctctca attattgaga tctg 24
E--> 362 <210> SEQ ID NO: 20
363 <211> LENGTH: 30
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial
367 <220> FEATURE:
368 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
E--> 370 <400> SEQUENCE: 20
371 gcgggatcca ccatgtctct tcaacaagta 30
E--> 374 <210> SEQ ID NO: 21
375 <211> LENGTH: 30
376 <212> TYPE: DNA
377 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING DATE: 01/10/2006
PATENT APPLICATION: **US/10/520,033** TIME: 08:16:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

379 <220> FEATURE:
380 <223> OTHER INFORMATION: Oligonucleotide having Sac I site
E--> **382 <400> SEQUENCE: 21**
383 gccgagctct tagaactcca accacttttg 30
E--> **386 <210> ~~SEQ ID NO.~~22**
387 <211> LENGTH: 27
388 <212> TYPE: DNA
389 <213> ORGANISM: Artificial
391 <220> FEATURE:
392 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
E--> **394 <400> SEQUENCE: 22**
395 ggcggatccg tctcccagtt gttcttc 27
E--> **398** 7 delete

VERIFICATION SUMMARY DATE: 01/10/2006
PATENT APPLICATION: **US/10/520,033** TIME: 08:16:22

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:47 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:52 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2
L:78 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:89 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3
L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:142 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
L:146 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:155 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5
L:159 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:168 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6
L:172 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:181 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
L:185 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:194 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8
L:198 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:206 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9
L:210 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:215 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10
L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:260 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11
L:264 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:273 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12
L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:285 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13
L:289 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:297 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14
L:301 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15
L:314 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:322 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:334 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17
L:338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:346 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18
L:350 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:358 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19
L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:370 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20
L:374 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21
L:386 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:394 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22
L:398 M:254 E: No. of Bases conflict, this line has no nucleotides.